

AMENDMENTS TO THE SPECIFICATION:

Please amend the specification accordingly.

Amend the first paragraph on page 10 as follows:

(B) Amino acid sequences of the chimeric polypeptides at the fusion sites, PV-PV (SEQ ID NO: 18); -PVIII (SEQ ID NO: 19); ELBI-PV (SEQ ID NO: 20); MoK-PV (SEQ ID NO: 21); PV-MoK (SEQ ID NO: 22); MoK-Sad (SEQ ID NO: 23). The linear region carrying epitope VI (amino acid 264) is indicated by underlining at residues 251-275. Black and gray boxes outline the EBL-1 and Mok sequences, respectively.

Dashes represent amino acids similar to those of the PV sequence, and dots represent gaps.

Amend the fourth paragraph on page 10 as follows:

(E) Comparison of the deduced amino acid sequences of G proteins of selected lyssaviruses, PV (SEQ ID NO: 24); USA7-BT (SEQ ID NO: 25); PI (SEQ ID NO: 26); EBLIPOL (SEQ ID NO: 27); EBLIFRA (SEQ ID NO: 28); EBL2FIN (SEQ ID NO: 29); EBL2HOL (SEQ ID NO: 30); Duv1SAF (SEQ ID NO: 31); Duv2SAF (SEQ ID NO: 32); Lag1NGA (SEQ ID NO: 33); Lag2CAR (SEQ ID NO: 34); Mok3ETP (SEQ ID NO: 35); Mok2ZIM (SEQ ID NO: 36). The consensus sequence is presented as the bottom sequence. Light grey boxes indicate the main antigenic sites. Dark grey boxes indicate the hydrophobic signal peptide (SP) and the transmembrane domain (TM). Underlined NX(S/T) motifs are potential N-glycosylation sites.